

OIEP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/003,690

DATE: 12/11/2001  
TIME: 11:50:00

Input Set : A:\Seqlist.txt  
Output Set: N:\CRF3\12112001\I003690.raw

4 <110> APPLICANT: Rory A.J. Curtis  
6 <120> TITLE OF INVENTION: 55053, A Novel Human Eukaryotic Kinase  
7 and Uses Therefor  
9 <130> FILE REFERENCE: MNI-206  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/003,690  
C--> 11 <141> CURRENT FILING DATE: 2001-11-15  
11 <150> PRIOR APPLICATION NUMBER: 60/248,893  
12 <151> PRIOR FILING DATE: 2000-11-15  
14 <160> NUMBER OF SEQ ID NOS: 8  
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 2980  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Homo sapiens  
23 <220> FEATURE:  
24 <221> NAME/KEY: CDS  
25 <222> LOCATION: (86)...(2419)  
27 <400> SEQUENCE: 1  
28 gtcgacccac gcgtccgcgg acgcgtgggc ggacgcgtgg gcggacgcgt gggggggggac 60  
29 cggtcggggcc gggaccaagg gcacc atg tcg tcc ggg gcc aag gag gga ggt 112  
30 Met Ser Ser Gly Ala Lys Glu Gly Gly  
31 1 5  
33 ggg ggc tct ccc gcc tac cac ctc ccc cac ccc cac cca ccc 160  
34 Gly Gly Ser Pro Ala Tyr His Leu Pro His Pro His Pro Pro  
35 10 15 20 25  
37 cag cac gcc caa tat gtg ggc ccc tat cgg ctg gag aag acg ctg ggc 208  
38 Gln His Ala Gln Tyr Val Gly Pro Tyr Arg Leu Glu Lys Thr Leu Gly  
39 30 35 40  
41 aaa gga cag aca ggg ctg gtt aaa ctc ggg gtc cac tgc atc acg ggt 256  
42 Lys Gly Gln Thr Gly Leu Val Lys Leu Gly Val His Cys Ile Thr Gly  
43 45 50 55  
45 cag aag gtc gcc atc aag atc gtg aac cgg gag aag ctg tcg gag tcg 304  
46 Gln Lys Val Ala Ile Lys Ile Val Asn Arg Glu Lys Leu Ser Glu Ser  
47 60 65 70  
49 gtg ctg atg aag gtg gag cgg gag atc gcc atc ctg aag ctc atc gaa 352  
50 Val Leu Met Lys Val Glu Arg Glu Ile Ala Ile Leu Lys Leu Ile Glu  
51 75 80 85  
53 cac cca cat gtc ctc aag ctc cac gac gtc tac gag aac aag aaa tat 400  
54 His Pro His Val Leu Lys Leu His Asp Val Tyr Glu Asn Lys Lys Tyr  
55 90 95 100 105  
57 ttg tac ctg gtt ctg gag cac gtc tcg ggg ggt gag cta ttc gac tac 448  
58 Leu Tyr Leu Val Leu Glu His Val Ser Gly Gly Glu Leu Phe Asp Tyr  
59 110 115 120  
61 ctg gta aag aag ggg aga ctg acg ccc aag gag gcc cga aag ttc ttc 496  
62 Leu Val Lys Lys Gly Arg Leu Thr Pro Lys Glu Ala Arg Lys Phe Phe  
63 125 130 135  
65 cgc cag att gtg tct gcg ctg gac ttc tgc cac agc tac tcc atc tgc 544

ENTERED

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66 Arg Gln Ile Val Ser Ala Leu Asp Phe Cys His Ser Tyr Ser Ile Cys
67      140      145      150
69 cac aga gac cta aag ccc gag aac ctg ctt ttg gat gag aaa aac aac 592
70 His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn
71      155      160      165
73 atc cgc att gca gac ttc ggc atg gcg tcc ctg cag gtg ggg gac agc 640
74 Ile Arg Ile Ala Asp Phe Gly Met Ala Ser Leu Gln Val Gly Asp Ser
75 170      175      180      185
77 ctc ctg gag acc agc tgc ggg tcc ccc cat tat gcg tgt cca gag gtg 688
78 Leu Leu Glu Thr Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu Val
79      190      195      200
81 att aag ggg gaa aaa tat gat ggc cgc cgg gca gac atg tgg agc tgt 736
82 Ile Lys Gly Glu Lys Tyr Asp Gly Arg Arg Ala Asp Met Trp Ser Cys
83      205      210      215
85 gga gtc atc ctc ttc gcc ctg ctc gtg ggg gct ctg ccc ttt gat gac 784
86 Gly Val Ile Leu Phe Ala Leu Leu Val Gly Ala Leu Pro Phe Asp Asp
87      220      225      230
89 gac aac ctc cgc cag ctg ctg gag aag gtg aaa cgg ggc gtc ttc cac 832
90 Asp Asn Leu Arg Gln Leu Leu Glu Lys Val Lys Arg Gly Val Phe His
91      235      240      245
93 atg ccc cac ttc att cct cca gat tgc cag agc ctc ctg agg gga atg 880
94 Met Pro His Phe Ile Pro Pro Asp Cys Gln Ser Leu Leu Arg Gly Met
95 250      255      260      265
97 atc gaa gtg gag ccc gaa aaa agg ctc agt ctg gag caa att cag aaa 928
98 Ile Glu Val Glu Pro Glu Lys Arg Leu Ser Leu Glu Gln Ile Gln Lys
99      270      275      280
101 cat cct tgg tac cta ggc ggg aaa cac gag cca gac ccg tgc ctg gag 976
102 His Pro Trp Tyr Leu Gly Gly Lys His Glu Pro Asp Pro Cys Leu Glu
103      285      290      295
105 cca gcc cct ggc cgc cgg gta gcc atg cgg agc ctg cca tcc aac gga 1024
106 Pro Ala Pro Gly Arg Arg Val Ala Met Arg Ser Leu Pro Ser Asn Gly
107      300      305      310
109 gag ctg gac ccc gac gtc cta gag agc atg gca tca ctg ggc tgc ttc 1072
110 Glu Leu Asp Pro Asp Val Leu Glu Ser Met Ala Ser Leu Gly Cys Phe
111      315      320      325
113 agg gac cgc gag agg ctg cat cgc gag ctg cgc agt gag gag gag aac 1120
114 Arg Asp Arg Glu Arg Leu His Arg Glu Leu Arg Ser Glu Glu Glu Asn
115 330      335      340      345
117 caa gaa aag atg ata tat tat ctg ctt ttg gat cgg aag gag cgg tat 1168
118 Gln Glu Lys Met Ile Tyr Tyr Leu Leu Leu Asp Arg Lys Glu Arg Tyr
119      350      355      360
121 ccc agc tgt gag gac cag gac ctg cct ccc cgg aat gat gtt gac ccc 1216
122 Pro Ser Cys Glu Asp Gln Asp Leu Pro Pro Arg Asn Asp Val Asp Pro
123      365      370      375
125 ccc cgg aag cgt gtg gat tct ccc atg ctg agc cgt cac ggg aag cgg 1264
126 Pro Arg Lys Arg Val Asp Ser Pro Met Leu Ser Arg His Gly Lys Arg
127      380      385      390
129 cga cca gag cgg aag tcc atg gaa gtc ctg agc atc acc gat gcc ggg 1312
130 Arg Pro Glu Arg Lys Ser Met Glu Val Leu Ser Ile Thr Asp Ala Gly

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131	395	400	405		
133	ggt ggt ggc tcc cct gta	ccc acc cga cgg gcc ttg	gag atg gcc cag	1360	
134	Gly Gly Gly Ser Pro Val	Pro Thr Arg Arg Ala Leu	Glu Met Ala Gln		
135	410	415	420	425	
137	cac agc cag aga tcc cgt	agc gtc agt gga gcc tcc	acg ggt ctg tcc	1408	
138	His Ser Gln Arg Ser Arg	Ser Val Ser Gly Ala Ser	Thr Gly Leu Ser		
139		430	435	440	
141	tcc agc cct cta agc agc	cca agg agt ccg gtc ttt	tcc ttt tca ccg	1456	
142	Ser Ser Pro Leu Ser Ser	Pro Arg Ser Pro Val Phe	Ser Phe Ser Pro		
143		445	450	455	
145	gag ccg ggg gct gga gat	gag gct cga ggc ggg ggc	tcc ccg act tcc	1504	
146	Glu Pro Gly Ala Gly Asp	Glu Ala Arg Gly Gly Gly	Ser Pro Thr Ser		
147		460	465	470	
149	aaa acg cag acg ctg cct	tct cgg ggc ccc agg ggt	ggg ggc gcc ggg	1552	
150	Lys Thr Gln Thr Leu Pro	Ser Arg Gly Pro Arg Gly	Gly Gly Ala Gly		
151		475	480	485	
153	gag cag ccc ccg ccc ccc	agt gcc cgc tcc aca ccc	ctg ccc ggc ccc	1600	
154	Glu Gln Pro Pro Pro Pro	Ser Ala Arg Ser Thr Pro	Leu Pro Gly Pro		
155	490	495	500	505	
157	cca ggc tcc ccg cgc tcc	tct ggc ggg acc ccc ttg	cac tcg cct ctg	1648	
158	Pro Gly Ser Pro Arg Ser	Ser Ser Gly Gly Thr Pro	Leu His Ser Pro		
159		510	515	520	
161	cac acg ccc cgg gcc agt	ccc acc ggg acc ccg ggg	aca aca cca ccc	1696	
162	His Thr Pro Arg Ala Ser	Pro Thr Gly Thr Pro Gly	Thr Thr Pro Pro		
163		525	530	535	
165	ccc agc ccc ggc ggt ggc	gtc ggg gga gcc gcc tgg	agg agt cgt ctc	1744	
166	Pro Ser Pro Gly Gly Gly	Val Gly Gly Ala Ala Trp	Arg Ser Arg Leu		
167		540	545	550	
169	aac tcc atc cgc aac agc	ttc ctg ggc tcc cct cgc	ttt cac cgg cgc	1792	
170	Asn Ser Ile Arg Asn Ser	Phe Leu Gly Ser Pro Arg	Phe His Arg Arg		
171		555	560	565	
173	aag atg cag gtc cct acc	gct gag gag atg tcc agc	ttg acg cca gag	1840	
174	Lys Met Gln Val Pro Thr	Ala Glu Glu Met Ser Ser	Leu Thr Pro Glu		
175	570	575	580	585	
177	tcc tcc ccg gag ctg gca	aaa cgc tcc tgg ttc ggg	aac ttc atc tcc	1888	
178	Ser Ser Pro Glu Leu Ala	Lys Arg Ser Trp Phe Gly	Asn Phe Ile Ser		
179		590	595	600	
181	ttg gac aaa gaa gaa caa	ata ttc ctc gtg cta aag	gac aaa cct ctc	1936	
182	Leu Asp Lys Glu Glu Gln	Ile Phe Leu Val Leu Lys	Asp Lys Pro Leu		
183		605	610	615	
185	agc agc atc aaa gca gac	atc gtc cat gcc ttt ctg	tcg atc ccc agc	1984	
186	Ser Ser Ile Lys Ala Asp	Ile Val His Ala Phe Leu	Ser Ile Pro Ser		
187		620	625	630	
189	ctg agt cac agt gtg ctg	tca cag acc agc ttc agg	gcc gag tac aag	2032	
190	Leu Ser His Ser Val Leu	Ser Gln Thr Ser Phe Arg	Ala Glu Tyr Lys		
191		635	640	645	
193	gcc agt ggc ggc ccc tcc	gtc ttc caa aag ccc gtc	cgc ttc cag gtg	2080	
194	Ala Ser Gly Gly Pro Ser	Val Phe Gln Lys Pro Val	Arg Phe Gln Val		
195	650	655	660	665	

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```

197 gac atc agc tcc tct gag ggt cca gag ccc tcc ccg cga cgg gac ggc 2128
198 Asp Ile Ser Ser Ser Glu Gly Pro Glu Pro Ser Pro Arg Arg Asp Gly
199 670 675 680
201 agc gga ggt ggt ggc atc tac tcc gtc acc ttc act ctc atc tcg ggt 2176
202 Ser Gly Gly Gly Gly Ile Tyr Ser Val Thr Phe Thr Leu Ile Ser Gly
203 685 690 695
205 ccc agc cgt cgg ttc aag cga gtg gtg gag acc atc cag gca cag ctc 2224
206 Pro Ser Arg Arg Phe Lys Arg Val Val Glu Thr Ile Gln Ala Gln Leu
207 700 705 710
209 ctg agc act cat gac cag ccc tcc gtg cag gcc ctg gca gac gag aag 2272
210 Leu Ser Thr His Asp Gln Pro Ser Val Gln Ala Leu Ala Asp Glu Lys
211 715 720 725
213 aac ggg gcc cag acc cgg cct gct ggt gcc cca ccc cga agc ctg cag 2320
214 Asn Gly Ala Gln Thr Arg Pro Ala Gly Ala Pro Pro Arg Ser Leu Gln
215 730 735 740 745
217 ccc cca ccc ggc cgc cca gac cca gag ctg agc agc tct ccc cgc cga 2368
218 Pro Pro Pro Gly Arg Pro Asp Pro Glu Leu Ser Ser Ser Pro Arg Arg
219 750 755 760
221 ggc ccc ccc aag gac aag aag ctc ctg gcc acc aac ggg acc cct ctg 2416
222 Gly Pro Pro Lys Asp Lys Lys Leu Leu Ala Thr Asn Gly Thr Pro Leu
223 765 770 775
225 ccc tgacccccacg gggccgggga gggaggggac cccctccac ccccttccg 2469
226 Pro
229 tgccccccaa ctgtgaatct gtaaataagg cccaaggaac atgtcgggag ggggggtggac 2529
230 acaaaaaccg gccttgccct gcagggatgg ggctccacag gccgtgcca actgggggtg 2589
231 gttctagggg aacagggggc gggggagctg tttctatattt atttattgat taatttatta 2649
232 ttttatttat tgatcaatct ctctgcgggg tgggggtgggg gagggacggg agctggttg 2709
233 ggtggttag cagatccgga cagggccctc tgtccctgtg tcgtcccca cccctcttc 2769
234 ccgggccct cctcccttg tctccccc acgaccttct gtacggattt gctctccgga 2829
235 aggaattctg gtttcgcgtg atcctgctg cgtccgtgtc tctgattccg ccggcggcaa 2889
236 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa ataataataa taaatagcct tgatcaggga 2949
237 aaaaaaaaaa aaaaaaaaaa ggcggccgct a 2980
239 <210> SEQ ID NO: 2
240 <211> LENGTH: 778
241 <212> TYPE: PRT
242 <213> ORGANISM: Homo sapiens
244 <400> SEQUENCE: 2
245 Met Ser Ser Gly Ala Lys Glu Gly Gly Gly Gly Ser Pro Ala Tyr His
246 1 5 10 15
247 Leu Pro His Pro His Pro His Pro Pro Gln His Ala Gln Tyr Val Gly
248 20 25 30
249 Pro Tyr Arg Leu Glu Lys Thr Leu Gly Lys Gly Gln Thr Gly Leu Val
250 35 40 45
251 Lys Leu Gly Val His Cys Ile Thr Gly Gln Lys Val Ala Ile Lys Ile
252 50 55 60
253 Val Asn Arg Glu Lys Leu Ser Glu Ser Val Leu Met Lys Val Glu Arg
254 65 70 75 80
255 Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro His Val Leu Lys Leu
256 85 90 95

```

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```

257 His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr Leu Val Leu Glu His
258              100              105              110
259 Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val Lys Lys Gly Arg Leu
260              115              120              125
261 Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln Ile Val Ser Ala Leu
262              130              135              140
263 Asp Phe Cys His Ser Tyr Ser Ile Cys His Arg Asp Leu Lys Pro Glu
264 145              150              155              160
265 Asn Leu Leu Leu Asp Glu Lys Asn Asn Ile Arg Ile Ala Asp Phe Gly
266              165              170              175
267 Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly
268              180              185              190
269 Ser Pro His Tyr Ala Cys Pro Glu Val Ile Lys Gly Glu Lys Tyr Asp
270              195              200              205
271 Gly Arg Arg Ala Asp Met Trp Ser Cys Gly Val Ile Leu Phe Ala Leu
272              210              215              220
273 Leu Val Gly Ala Leu Pro Phe Asp Asp Asp Asn Leu Arg Gln Leu Leu
274 225              230              235              240
275 Glu Lys Val Lys Arg Gly Val Phe His Met Pro His Phe Ile Pro Pro
276              245              250              255
277 Asp Cys Gln Ser Leu Leu Arg Gly Met Ile Glu Val Glu Pro Glu Lys
278              260              265              270
279 Arg Leu Ser Leu Glu Gln Ile Gln Lys His Pro Trp Tyr Leu Gly Gly
280              275              280              285
281 Lys His Glu Pro Asp Pro Cys Leu Glu Pro Ala Pro Gly Arg Arg Val
282              290              295              300
283 Ala Met Arg Ser Leu Pro Ser Asn Gly Glu Leu Asp Pro Asp Val Leu
284 305              310              315              320
285 Glu Ser Met Ala Ser Leu Gly Cys Phe Arg Asp Arg Glu Arg Leu His
286              325              330              335
287 Arg Glu Leu Arg Ser Glu Glu Glu Asn Gln Glu Lys Met Ile Tyr Tyr
288              340              345              350
289 Leu Leu Leu Asp Arg Lys Glu Arg Tyr Pro Ser Cys Glu Asp Gln Asp
290              355              360              365
291 Leu Pro Pro Arg Asn Asp Val Asp Pro Pro Arg Lys Arg Val Asp Ser
292              370              375              380
293 Pro Met Leu Ser Arg His Gly Lys Arg Arg Pro Glu Arg Lys Ser Met
294 385              390              395              400
295 Glu Val Leu Ser Ile Thr Asp Ala Gly Gly Gly Gly Ser Pro Val Pro
296              405              410              415
297 Thr Arg Arg Ala Leu Glu Met Ala Gln His Ser Gln Arg Ser Arg Ser
298              420              425              430
299 Val Ser Gly Ala Ser Thr Gly Leu Ser Ser Ser Pro Leu Ser Ser Pro
300              435              440              445
301 Arg Ser Pro Val Phe Ser Phe Ser Pro Glu Pro Gly Ala Gly Asp Glu
302              450              455              460
303 Ala Arg Gly Gly Gly Ser Pro Thr Ser Lys Thr Gln Thr Leu Pro Ser
304 465              470              475              480
305 Arg Gly Pro Arg Gly Gly Gly Ala Gly Glu Gln Pro Pro Pro Pro Ser

```

→ Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\Seqlist.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:582 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4